IN THE CLAIMS:

1-2. (canceled)

3. (currently amended) A method of selectively detecting human papillomavirus (HPV) ~~genome~~ genotypes, comprising performing a polymerase chain reaction for genomic DNA contained in a biological sample using ~~one or more~~ each of the primer pairs ~~selected from among pairs of primers capable of complementarily binding to the HPV genome and~~ having nucleotide sequences represented by SEQ ID Nos. 1 and 2, SEQ ID Nos. 3 and 4, SEQ ID Nos. 5 and 6, and SEQ ID Nos. 7 and 8, wherein each primer pair binds and specifically amplifies specific regions of the L 1 gene of each of the human papillomavirus (HPV) genotypes HPV 11, HPV 16, HPV 18 and HPV 31, and wherein the primers specifically and selectively amplify each of the four different HPV genotypes when said genotypes are present at a copy number of 62.5 or greater in said biological sample.

4. (original) The method as set forth in claim 3, wherein an HPV 11 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 1 and 2.

5. (original) The method as set forth in claim 3, wherein an HPV 16 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 3 and 4.

6. (original) The method as set forth in claim 3, wherein an HPV 18 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 5 and 6.

7. (original) The method as set forth in claim 3, wherein an HPV 31 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 7 and 8.

8. (canceled)